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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Aug 03 11:25:30 EDT 2007

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Reviewer Comments:

<210> 2

<211> 1209

<212> DNA

<213> Unknown

<220>

<223> environmental sample

<221> misc_feature

<222> 734

<223> n = A, T, C or G

<400> 2

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120

ctcggcttt tcgcccattcc ggcgctggat gaagaaaaatc cagacggccc ggttcataat
180

ttcgcgcctt tagaccaaatt tgctgccctg aaatgggtgc aggaaaatat cgctgcttc
240

ggcggcgacg cgggaaatgt cacgctgttt ggcgagtctg ccggggcgcg tagcgtgctt
300

tcgctgctgg cgtcgccgct ggcgaaaaac ctttccaca aaggtattat acaaagcgcc
360

tacacgttgc cggatgtcga caggaagaaa gccctgaaac gtggcgtagc gctggccggt
420

cattacgggc tgcaaatgc cacagcggat gaactccgca ctctgcctgc ggatggctg
480

tgggcgcttg aaggcccgct taacatttgtt ccaacgccaa tctccggcga cgtcggtcg
 540
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 600
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 720
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 780
 nccncgctgg gttttgttgt gatgcaggcc cagcagcggg tcaatcagcc ctgctggcgc
 840

The above <222> response only indicates one "n" location (734); however, n's are also located at 781 and 784: please explain them.

(from Sequence 3)

<221> VARIANT
 <222> 245, 260, 261
 <223> Xaa = Any Amino Acid

<400> 3
 Met Val Trp Leu His Gly Gly Tyr Thr Ile Gly Ala Gly Ser Leu
 1 5 10 15
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 20 25 30
 Thr Val Asn Tyr Arg Leu Gly His Leu Gly Phe Phe Ala His Pro Ala
 35 40 45
 Leu Asp Glu Glu Asn Pro Asp Gly Pro Val His Asn Phe Ala Leu Leu
 50 55 60
 Asp Gln Ile Ala Ala Leu Lys Trp Val Gln Glu Asn Ile Ala Ala Phe
 65 70 75 80
 Gly Gly Asp Ala Gly Asn Val Thr Leu Phe Gly Glu Ser Ala Gly Ala
 85 90 95
 Arg Ser Val Leu Ser Leu Leu Ala Ser Pro Leu Ala Lys Asn Leu Phe
 100 105 110
 His Lys Gly Ile Ile Gln Ser Ala Tyr Thr Leu Pro Asp Val Asp Arg
 115 120 125
 Lys Lys Ala Leu Lys Arg Gly Val Ala Leu Ala Gly His Tyr Gly Leu
 130 135 140
 Gln Asn Ala Thr Ala Asp Glu Leu Arg Ala Leu Pro Ala Asp Gly Leu

| | | | |
|---|-----|-----|-----|
| 145 | 150 | 155 | 160 |
| Trp Ala Leu Glu Gly Pro Leu Asn Ile Gly Pro Thr Pro Ile Ser Gly | | | |
| 165 | 170 | | 175 |
| Asp Val Val Leu Pro Glu Pro Met Leu Asp Ile Phe Phe Ala Gly Arg | | | |
| 180 | 185 | | 190 |
| Gln His Arg Met Pro Leu Met Val Gly Ser Asn Ser Asp Glu Ala Ser | | | |
| 195 | 200 | 205 | |
| Val Leu Ser Tyr Phe Gly Ile Asp Pro Ala Gly Gln Val Glu Leu Leu | | | |
| 210 | 215 | 220 | |
| Arg Arg Gly Ala Ala Phe Pro Asp Trp Gly Leu Ile Lys Leu Leu Tyr | | | |
| 225 | 230 | 235 | 240 |
| Ser Arg Ser Glu Xaa Gly Met Pro Glu Leu Gly Arg Gln Val Cys Arg | | | |
| 245 | 250 | | 255 |
| Asp Met Ala Phe Xaa Xaa Leu Gly Phe Val Val Met Gln Ala Gln Gln | | | |
| 260 | 265 | 270 | |

The above <222> response is incorrect: while Xaa is located at 245, "Phe" is located at 260 (not Xaa). Xaa's are located at 261 and 262.

Application No: 10555587 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-01 10:04:38.617
Finished: 2007-08-01 10:04:39.579
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 962 ms
Total Warnings: 3
Total Errors: 8
No. of SeqIDs Defined: 3
Actual SeqID Count: 3

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| E 342 | 'n' position not defined found at POS: 1926 SEQID(1) |
| E 342 | 'n' position not defined found at POS: 1973 SEQID(1) |
| E 342 | 'n' position not defined found at POS: 1976 SEQID(1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| E 342 | 'n' position not defined found at POS: 781 SEQID(2) |
| E 342 | 'n' position not defined found at POS: 784 SEQID(2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| E 341 | 'Xaa' position not defined SEQID (3) POS (245) |
| E 341 | 'Xaa' position not defined SEQID (3) POS (261) |
| E 341 | 'Xaa' position not defined SEQID (3) POS (262) |

SEQUENCE LISTING

<110> Genencor International, Inc.

Jones, Brian E.

Grant, William D.

Heaphy, Shaun

Rees, Helen C.

Grant, Susan

<120> Novel Lipolytic Enzyme LIP1

<130> GC801-2-PCT

<140> 10555587

<141> 2007-08-01

<150> PCT/US04/014752

<151> 2004-05-12

<150> US 60/469,931

<151> 2003-05-12

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4313

<212> DNA

<213> Unknown

<220>

<223> environmental sample

<221> misc_feature

<222> 1926, 1973, 1976

<223> n = A,T,C or G

<400> 1

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| atgatgagca cccgctgatc gcccgtatgtatc tctgcttccg tggctgccac attaaccacc | 180 |
| tgaccccgcg cacgctcgat atcgaccgcg tgcaagtgcgt gatgccggaa cgccggaaatta | 240 |
| ccccaaagc cattatcgaa gggccgcgcg gcccgcggcg cccgatttttta ctgcgcggaga | 300 |
| ccagctttaa agcgctggaa gagcctattt tgttccggcg tgagcatcac ggaacgcata | 360 |
| ccgccccgtt cggcgaaata gaacagcgcg gcgttagcgct gacgcccggaa ggccggggcg | 420 |
| tgtacgacga actgctgctg gcccggggca acggcacggta taatctcagc caccagcagc | 480 |
| atttacacga agtgttcacc gttcccgaa cagcgacgcg ctgctgcgcg cccaggggct | 540 |
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<213> Unknown

<220>
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<221> misc_feature
<222> 734
<223> n = A,T,C or G

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| ctcggtttt | tcgcccattcc | ggcgctggat | gaagaaaatc | cagacggccc | ggttcataat | 180 |
| ttcgcgttt | tagaccaaatt | tgcgtccctg | aatgggtgc | aggaaaatat | cgctgcttc | 240 |
| ggcggcgacg | cggggaaatgt | cacgctgttt | ggcgagtctg | ccggggcgcg | tagcgtgctt | 300 |
| tcgctgtgg | cgtcgccgct | ggcgaaaaac | ctttccaca | aaggtattat | acaaagcgcc | 360 |
| tacacgttgc | cggatgtcga | caggaagaaa | gccctgaaac | gtggcgttagc | gctggccggt | 420 |
| cattacgggc | tgcaaaatgc | cacagcggat | gaactcccg | ctctgcctgc | ggatggctg | 480 |
| tgggcgttg | aaggcccgt | taacatttgt | ccaacgcca | tctccggcga | cgtcgtgctg | 540 |
| cctgagccga | tgctggatat | attttcgcc | gggcgtcage | accgcattgc | cttgcgtggc | 600 |
| gggagcaaca | gcgacgaggc | aagcgtgctg | agctacttcg | gcatcgatcc | tgccggcag | 660 |
| gtcgaactgc | tgcgcgggg | agcggcgctt | ccggactggg | ggcttatcaa | actgctgtat | 720 |
| tcccgagtg | aaangggat | gcccgaactc | gggcgacagg | tgtgcgcga | tatggcttt | 780 |
| ncncgctgg | gttttgtgt | gatgcaggcc | cagcagcggg | tcaatcagcc | ctgctggcgc | 840 |
| tactatttt | attatgtggg | ggagggcgaa | cgtaaaatct | atgcacacgg | cacctggcac | 900 |
| ggcaacgaag | tgcgtatgt | tttgacacg | ttaagtcga | cgccacccgc | aagtgaatac | 960 |
| gtcaaccaaa | acgatctcac | gttgcgggg | caaatttgt | actactggac | ccgtttgcc | 1020 |
| cgcagcgccc | gtccccacag | taaagcgata | ccgggcccgc | taagctggcc | tgcctgcgtt | 1080 |
| cgcggcaagg | accgaacgat | gcggtaggc | gttcactcgc | ggcgcgggtt | caaagtggaa | 1140 |
| aaccgctta | tgcgcattag | aatgcagctg | tttaagcggg | tcatgaagca | tcacgtcagc | 1200 |
| cttgcactga | | | | | | 1209 |

<210> 3
<211> 402
<212> PRT
<213> Unknown

<220>
<223> environmental sample

<221> VARIANT
<222> 245, 260, 261
<223> Xaa = Any Amino Acid

<400> 3

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| 1 | | | | | 5 | | | 10 | | | | 15 | | | |
| Pro | Pro | Tyr | Asp | Gly | Ala | Ala | Phe | Ala | Ser | Arg | Asp | Val | Val | Leu | Val |
| | | | | | | | | 20 | | | 25 | | | 30 | |
| Thr | Val | Asn | Tyr | Arg | Leu | Gly | His | Leu | Gly | Phe | Phe | Ala | His | Pro | Ala |
| | | | | | | | | 35 | | | 40 | | | 45 | |
| Leu | Asp | Glu | Glu | Asn | Pro | Asp | Gly | Pro | Val | His | Asn | Phe | Ala | Leu | Leu |
| | | | | | | | | 50 | | | 55 | | | 60 | |
| Asp | Gln | Ile | Ala | Ala | Leu | Lys | Trp | Val | Gln | Glu | Asn | Ile | Ala | Ala | Phe |

| | 70 | | 75 | | 80 |
|---|-----|--|-----|--|-----|
| Gly Gly Asp Ala Gly Asn Val Thr Leu Phe Gly Glu Ser Ala Gly Ala | | | | | |
| | 85 | | 90 | | 95 |
| Arg Ser Val Leu Ser Leu Leu Ala Ser Pro Leu Ala Lys Asn Leu Phe | | | | | |
| | 100 | | 105 | | 110 |
| His Lys Gly Ile Ile Gln Ser Ala Tyr Thr Leu Pro Asp Val Asp Arg | | | | | |
| | 115 | | 120 | | 125 |
| Lys Lys Ala Leu Lys Arg Gly Val Ala Leu Ala Gly His Tyr Gly Leu | | | | | |
| | 130 | | 135 | | 140 |
| Gln Asn Ala Thr Ala Asp Glu Leu Arg Ala Leu Pro Ala Asp Gly Leu | | | | | |
| | 145 | | 150 | | 160 |
| Trp Ala Leu Glu Gly Pro Leu Asn Ile Gly Pro Thr Pro Ile Ser Gly | | | | | |
| | 165 | | 170 | | 175 |
| Asp Val Val Leu Pro Glu Pro Met Leu Asp Ile Phe Phe Ala Gly Arg | | | | | |
| | 180 | | 185 | | 190 |
| Gln His Arg Met Pro Leu Met Val Gly Ser Asn Ser Asp Glu Ala Ser | | | | | |
| | 195 | | 200 | | 205 |
| Val Leu Ser Tyr Phe Gly Ile Asp Pro Ala Gly Gln Val Glu Leu Leu | | | | | |
| | 210 | | 215 | | 220 |
| Arg Arg Gly Ala Ala Phe Pro Asp Trp Gly Leu Ile Lys Leu Leu Tyr | | | | | |
| | 225 | | 230 | | 240 |
| Ser Arg Ser Glu Xaa Gly Met Pro Glu Leu Gly Arg Gln Val Cys Arg | | | | | |
| | 245 | | 250 | | 255 |
| Asp Met Ala Phe Xaa Xaa Leu Gly Phe Val Val Met Gln Ala Gln Gln | | | | | |
| | 260 | | 265 | | 270 |
| Arg Val Asn Gln Pro Cys Trp Arg Tyr Tyr Phe Asp Tyr Val Gly Glu | | | | | |
| | 275 | | 280 | | 285 |
| Ala Glu Arg Lys Ile Tyr Ala Asn Gly Thr Trp His Gly Asn Glu Val | | | | | |
| | 290 | | 295 | | 300 |
| Pro Tyr Val Phe Asp Thr Leu Ser Leu Thr Pro Pro Ala Ser Glu Tyr | | | | | |
| | 305 | | 310 | | 320 |
| Val Asn Gln Asn Asp Leu Thr Phe Ala Gly Gln Ile Cys Asp Tyr Trp | | | | | |
| | 325 | | 330 | | 335 |
| Thr Arg Phe Ala Arg Ser Ala Gly Pro His Ser Lys Ala Ile Pro Gly | | | | | |
| | 340 | | 345 | | 350 |
| Pro Leu Ser Trp Pro Ala Cys Val Arg Gly Lys Asp Arg Thr Met Arg | | | | | |
| | 355 | | 360 | | 365 |
| Leu Gly Val His Ser Arg Ala Arg Phe Lys Val Glu Asn Arg Phe Met | | | | | |
| | 370 | | 375 | | 380 |
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| | 385 | | 390 | | 400 |
| Leu Asp | | | | | |